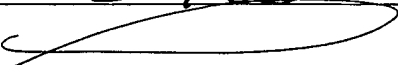


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The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/5261061
Source: PST
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PATENT APPLICATION: US/10/526,061

TIME: 15:15:33

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Output Set: N:\CRF4\03092005\J526061.raw

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3 <110> APPLICANT: KONDO, Naomi
4     MATSUI, Eiko
5     KANEKO, Hideo
6     AOKI, Minako
7     NAGAO, Mizuho
8     KASAHARA, Kimiko
9     TATEBAYASHI, Hiroharu
10    HATTORI, Hiroaki
11    EGASHIRA, Toru
13 <120> TITLE OF INVENTION: METHOD FOR DETECTING GENE SPECIFYING ALLERGIC PREDISPOSITION
15 <130> FILE REFERENCE: Q86473
C--> 17 <140> CURRENT APPLICATION NUMBER: US/10/526,061
C--> 17 <141> CURRENT FILING DATE: 2005-02-28
17 <150> PRIOR APPLICATION NUMBER: PCT/JP03/11118
18 <151> PRIOR FILING DATE: 2003-08-29
20 <150> PRIOR APPLICATION NUMBER: PCT/JP02/10018
21 <151> PRIOR FILING DATE: 2002-09-27
23 <150> PRIOR APPLICATION NUMBER: JP 2002-252446
24 <151> PRIOR FILING DATE: 2002-08-30
26 <160> NUMBER OF SEQ ID NOS: 69
28 <170> SOFTWARE: PatentIn version 3.3
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31 <211> LENGTH: 3400
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33 <213> ORGANISM: Homo sapiens
36 <220> FEATURE:
37 <221> NAME/KEY: exon
38 <222> LOCATION: (1)..(2589)
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43 1      5      10      15
45 acg tgg ctg ttg att aaa gca aaa ata gat gcg tgc aag aga ggc gat      96
46 Thr Trp Leu Leu Ile Lys Ala Lys Ile Asp Ala Cys Lys Arg Gly Asp
47      20      25      30
49 gtg act gtg aag cct tcc cat gta att tta ctt gga tcc act gtc aat      144
50 Val Thr Val Lys Pro Ser His Val Ile Leu Leu Gly Ser Thr Val Asn
51      35      40      45
53 att aca tgc tct ttg aag ccc aga caa ggc tgc ttt cac tat tcc aga      192
54 Ile Thr Cys Ser Leu Lys Pro Arg Gln Gly Cys Phe His Tyr Ser Arg
55      50      55      60
57 cgt aac aag tta atc ctg tac aag ttt gac aga aga atc aat ttt cac      240
58 Arg Asn Lys Leu Ile Leu Tyr Lys Phe Asp Arg Arg Ile Asn Phe His

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62	His	Gly	His	Ser	Leu	Asn	Ser	Gln	Val	Thr	Gly	Leu	Pro	Leu	Gly	Thr			
63					85					90					95				
65	acc	ttg	ttt	gtc	tgc	aaa	ctg	gcc	tgt	atc	aat	agt	gat	gaa	att	caa		336	
66	Thr	Leu	Phe	Val	Cys	Lys	Leu	Ala	Cys	Ile	Asn	Ser	Asp	Glu	Ile	Gln			
67				100					105					110					
69	ata	tgt	gga	gca	gag	atc	ttc	gtt	ggg	gtt	gct	cca	gaa	cag	cct	caa		384	
70	Ile	Cys	Gly	Ala	Glu	Ile	Phe	Val	Gly	Val	Ala	Pro	Glu	Gln	Pro	Gln			
71			115					120					125						
73	aat	tta	tcc	tgc	ata	cag	aag	gga	gaa	cag	ggg	act	gtg	gcc	tgc	acc		432	
74	Asn	Leu	Ser	Cys	Ile	Gln	Lys	Gly	Glu	Gln	Gly	Thr	Val	Ala	Cys	Thr			
75		130					135					140							
77	tgg	gaa	aga	gga	cga	gac	acc	cac	tta	tac	act	gag	tat	act	cta	cag		480	
78	Trp	Glu	Arg	Gly	Arg	Asp	Thr	His	Leu	Tyr	Thr	Glu	Tyr	Thr	Leu	Gln			
79	145					150					155				160				
81	cta	agt	gga	cca	aaa	aat	tta	acc	tgg	cag	aag	caa	tgt	aaa	gac	att		528	
82	Leu	Ser	Gly	Pro	Lys	Asn	Leu	Thr	Trp	Gln	Lys	Gln	Cys	Lys	Asp	Ile			
83				165					170				175						
85	tat	tgt	gac	tat	ttg	gac	ttt	gga	atc	aac	ctc	acc	cct	gaa	tca	cct		576	
86	Tyr	Cys	Asp	Tyr	Leu	Asp	Phe	Gly	Ile	Asn	Leu	Thr	Pro	Glu	Ser	Pro			
87			180						185				190						
89	gaa	tcc	aat	ttc	aca	gcc	aag	gtt	act	gct	gtc	aat	agt	ctt	gga	agc		624	
90	Glu	Ser	Asn	Phe	Thr	Ala	Lys	Val	Thr	Ala	Val	Asn	Ser	Leu	Gly	Ser			
91			195					200					205						
93	tcc	tct	tca	ctt	cca	tcc	aca	ttc	aca	ttc	ttg	gac	ata	gtg	agg	cct		672	
94	Ser	Ser	Ser	Leu	Pro	Ser	Thr	Phe	Thr	Phe	Leu	Asp	Ile	Val	Arg	Pro			
95		210					215					220							
97	ctt	cct	ccg	tgg	gac	att	aga	atc	aaa	ttt	caa	aag	gct	tcc	gtg	agc		720	
98	Leu	Pro	Pro	Trp	Asp	Ile	Arg	Ile	Lys	Phe	Gln	Lys	Ala	Ser	Val	Ser			
99	225					230				235					240				
101	aga	tgt	acc	ctt	tat	tgg	aga	gat	gag	gga	ctg	gta	ctg	ctt	aat	cga		768	
102	Arg	Cys	Thr	Leu	Tyr	Trp	Arg	Asp	Glu	Gly	Leu	Val	Leu	Leu	Asn	Arg			
103					245					250					255				
105	ctc	aga	tat	cgg	ccc	agt	aac	agc	agg	ctc	tgg	aat	atg	gtt	aat	gtt		816	
106	Leu	Arg	Tyr	Arg	Pro	Ser	Asn	Ser	Arg	Leu	Trp	Asn	Met	Val	Asn	Val			
107			260						265					270					
109	aca	aag	gcc	aaa	gga	aga	cat	gat	ttg	ctg	gat	ctg	aaa	cca	ttt	aca		864	
110	Thr	Lys	Ala	Lys	Gly	Arg	His	Asp	Leu	Leu	Asp	Leu	Lys	Pro	Phe	Thr			
111			275					280					285						
113	gaa	tat	gaa	ttt	cag	att	tcc	tct	aag	cta	cat	ctt	tat	aag	gga	agt		912	
114	Glu	Tyr	Glu	Phe	Gln	Ile	Ser	Ser	Lys	Leu	His	Leu	Tyr	Lys	Gly	Ser			
115		290					295					300							
117	tgg	agt	gat	tgg	agt	gaa	tca	ttg	aga	gca	caa	aca	cca	gaa	gaa	gag		960	
118	Trp	Ser	Asp	Trp	Ser	Glu	Ser	Leu	Arg	Ala	Gln	Thr	Pro	Glu	Glu	Glu			
119	305					310				315					320				
121	cct	act	ggg	atg	tta	gat	gtc	tgg	tac	atg	aaa	cgg	cac	att	gac	tac		1008	
122	Pro	Thr	Gly	Met	Leu	Asp	Val	Trp	Tyr	Met	Lys	Arg	His	Ile	Asp	Tyr			
123					325					330					335				

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126	Ser	Arg	Gln	Gln	Ile	Ser	Leu	Phe	Trp	Lys	Asn	Leu	Ser	Val	Ser	Glu	
127				340					345					350			
129	gca	aga	gga	aaa	att	ctc	cac	tat	cag	gtg	acc	ttg	cag	gag	ctg	aca	1104
130	Ala	Arg	Gly	Lys	Ile	Leu	His	Tyr	Gln	Val	Thr	Leu	Gln	Glu	Leu	Thr	
131			355					360						365			
133	gga	ggg	aaa	gcc	atg	aca	cag	aac	atc	aca	gga	cac	acc	tcc	tgg	acc	1152
134	Gly	Gly	Lys	Ala	Met	Thr	Gln	Asn	Ile	Thr	Gly	His	Thr	Ser	Trp	Thr	
135		370					375						380				
137	aca	gtc	att	cct	aga	acc	gga	aat	tgg	gct	gtg	gct	gtg	tct	gca	gca	1200
138	Thr	Val	Ile	Pro	Arg	Thr	Gly	Asn	Trp	Ala	Val	Ala	Val	Ser	Ala	Ala	
139	385					390					395					400	
141	aat	tca	aaa	ggc	agt	tct	ctg	ccc	act	cgt	att	aac	ata	atg	aac	ctg	1248
142	Asn	Ser	Lys	Gly	Ser	Ser	Leu	Pro	Thr	Arg	Ile	Asn	Ile	Met	Asn	Leu	
143				405						410				415			
145	tgt	gag	gca	ggg	ttg	ctg	gct	cct	cgc	cag	gtc	tct	gca	aac	tca	gag	1296
146	Cys	Glu	Ala	Gly	Leu	Leu	Ala	Pro	Arg	Gln	Val	Ser	Ala	Asn	Ser	Glu	
147			420						425					430			
149	ggc	atg	gac	aac	att	ctg	gtg	act	tgg	cag	cct	ccc	agg	aaa	gat	ccc	1344
150	Gly	Met	Asp	Asn	Ile	Leu	Val	Thr	Trp	Gln	Pro	Pro	Arg	Lys	Asp	Pro	
151			435					440						445			
153	tct	gct	gtt	cag	gag	tac	gtg	gtg	gaa	tgg	aga	gag	ctc	cat	cca	ggg	1392
154	Ser	Ala	Val	Gln	Glu	Tyr	Val	Val	Glu	Trp	Arg	Glu	Leu	His	Pro	Gly	
155		450					455						460				
157	ggt	gac	aca	cag	gtc	cct	cta	aac	tgg	cta	cgg	agt	cga	ccc	tac	aat	1440
158	Gly	Asp	Thr	Gln	Val	Pro	Leu	Asn	Trp	Leu	Arg	Ser	Arg	Pro	Tyr	Asn	
159	465					470					475				480		
161	gtg	tct	gct	ctg	att	tca	gag	aac	ata	aaa	tcc	tac	atc	tgt	tat	gaa	1488
162	Val	Ser	Ala	Leu	Ile	Ser	Glu	Asn	Ile	Lys	Ser	Tyr	Ile	Cys	Tyr	Glu	
163				485						490				495			
165	atc	cgt	gtg	tat	gca	ctc	tca	ggg	gat	caa	gga	gga	tgc	agc	tcc	atc	1536
166	Ile	Arg	Val	Tyr	Ala	Leu	Ser	Gly	Asp	Gln	Gly	Gly	Cys	Ser	Ser	Ile	
167			500						505					510			
169	ctg	ggt	aac	tct	aag	cac	aaa	gca	cca	ctg	agt	ggc	ccc	cac	att	aat	1584
170	Leu	Gly	Asn	Ser	Lys	His	Lys	Ala	Pro	Leu	Ser	Gly	Pro	His	Ile	Asn	
171			515					520						525			
173	gcc	atc	aca	gag	gaa	aag	ggg	agc	att	tta	att	tca	tgg	aac	agc	att	1632
174	Ala	Ile	Thr	Glu	Glu	Lys	Gly	Ser	Ile	Leu	Ile	Ser	Trp	Asn	Ser	Ile	
175		530					535							540			
177	cca	gtc	cag	gag	caa	atg	ggc	tgc	ctc	ctc	cat	tat	agg	ata	tac	tgg	1680
178	Pro	Val	Gln	Glu	Gln	Met	Gly	Cys	Leu	Leu	His	Tyr	Arg	Ile	Tyr	Trp	
179	545					550					555				560		
181	aag	gaa	cgg	gac	tcc	aac	tcc	cag	cct	cag	ctc	tgt	gaa	att	ccc	tac	1728
182	Lys	Glu	Arg	Asp	Ser	Asn	Ser	Gln	Pro	Gln	Leu	Cys	Glu	Ile	Pro	Tyr	
183				565						570				575			
185	aga	gtc	tcc	caa	aat	tca	cat	cca	ata	aac	agc	ctg	cag	ccc	cga	gtg	1776
186	Arg	Val	Ser	Gln	Asn	Ser	His	Pro	Ile	Asn	Ser	Leu	Gln	Pro	Arg	Val	
187			580						585					590			
189	aca	tat	gtc	ctg	tgg	atg	aca	gct	ctg	aca	gct	gct	ggt	gaa	agt	tcc	1824

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193	cac	gga	aat	gag	agg	gaa	ttt	tgt	ctg	caa	ggg	aaa	gcc	aat	tgg	atg	1872
194	His	Gly	Asn	Glu	Arg	Glu	Phe	Cys	Leu	Gln	Gly	Lys	Ala	Asn	Trp	Met	
195		610					615					620					
197	gcg	ttt	gtg	gca	cca	agc	att	tgc	att	gct	atc	atc	atg	gtg	ggc	att	1920
198	Ala	Phe	Val	Ala	Pro	Ser	Ile	Cys	Ile	Ala	Ile	Ile	Met	Val	Gly	Ile	
199	625					630				635						640	
201	ttc	tca	acg	cat	tac	ttc	cag	caa	aag	gtg	ttt	gtt	ctc	cta	gca	gcc	1968
202	Phe	Ser	Thr	His	Tyr	Phe	Gln	Gln	Lys	Val	Phe	Val	Leu	Leu	Ala	Ala	
203				645						650					655		
205	ctc	aga	cct	cag	tgg	tgt	agc	aga	gaa	att	cca	gat	cca	gca	aat	agc	2016
206	Leu	Arg	Pro	Gln	Trp	Cys	Ser	Arg	Glu	Ile	Pro	Asp	Pro	Ala	Asn	Ser	
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211			675				680					685					
213	ttg	gac	agg	ctc	ctg	ata	gac	tgg	ccc	acg	cct	gaa	gat	cct	gaa	ccg	2112
214	Leu	Asp	Arg	Leu	Leu	Ile	Asp	Trp	Pro	Thr	Pro	Glu	Asp	Pro	Glu	Pro	
215		690				695				700							
217	ctg	gtc	atc	agt	gaa	gtc	ctt	cat	caa	gtg	acc	cca	gtt	ttc	aga	cat	2160
218	Leu	Val	Ile	Ser	Glu	Val	Leu	His	Gln	Val	Thr	Pro	Val	Phe	Arg	His	
219	705				710					715					720		
221	ccc	ccc	tgc	tcc	aac	tgg	cca	caa	agg	gaa	aaa	gga	atc	caa	ggg	cat	2208
222	Pro	Pro	Cys	Ser	Asn	Trp	Pro	Gln	Arg	Glu	Lys	Gly	Ile	Gln	Gly	His	
223				725					730				735				
225	cag	gcc	tct	gag	aaa	gac	atg	atg	cac	agt	gcc	tca	agc	cca	cca	cct	2256
226	Gln	Ala	Ser	Glu	Lys	Asp	Met	Met	His	Ser	Ala	Ser	Ser	Pro	Pro	Pro	
227			740					745				750					
229	cca	aga	gct	ctc	caa	gct	gag	agc	aga	caa	ctg	gtg	gat	ctg	tac	aag	2304
230	Pro	Arg	Ala	Leu	Gln	Ala	Glu	Ser	Arg	Gln	Leu	Val	Asp	Leu	Tyr	Lys	
231		755				760					765						
233	gtg	ctg	gag	agc	agg	ggc	tcc	gac	cca	aag	cca	gaa	aac	cca	gcc	tgt	2352
234	Val	Leu	Glu	Ser	Arg	Gly	Ser	Asp	Pro	Lys	Pro	Glu	Asn	Pro	Ala	Cys	
235		770				775					780						
237	ccc	tgg	acg	gtg	ctc	cca	gca	ggg	gac	ctt	ccc	acc	cat	gat	ggc	tac	2400
238	Pro	Trp	Thr	Val	Leu	Pro	Ala	Gly	Asp	Leu	Pro	Thr	His	Asp	Gly	Tyr	
239	785				790				795						800		
241	tta	ccc	tcc	aac	ata	gat	gac	ctc	ccc	tca	cat	gag	gca	cct	ctc	gct	2448
242	Leu	Pro	Ser	Asn	Ile	Asp	Asp	Leu	Pro	Ser	His	Glu	Ala	Pro	Leu	Ala	
243				805					810					815			
245	gac	tct	ctg	gaa	gaa	ctg	gag	cct	cag	cac	atc	tcc	ctt	tct	gtt	ttc	2496
246	Asp	Ser	Leu	Glu	Glu	Leu	Glu	Pro	Gln	His	Ile	Ser	Leu	Ser	Val	Phe	
247			820					825					830				
249	ccc	tca	agt	tct	ctt	cac	cca	ctc	acc	ttc	tcc	tgt	ggg	gat	aag	ctg	2544
250	Pro	Ser	Ser	Ser	Leu	His	Pro	Leu	Thr	Phe	Ser	Cys	Gly	Asp	Lys	Leu	
251		835				840					845						
253	act	ctg	gat	cag	tta	aag	atg	agg	tgt	gac	tcc	ctc	atg	ctc	tga		2589
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261 tagaggacag gcaagccagc tctgggggag tcttaggaac tgggagttgg tcttcactca 2769
263 gatgcctcat cttgcctttc ccagggcctt aaaattacat ccttcactgt gtggacctag 2829
265 agactccaac ttgaattcct agtaactttc ttggtatgct ggccagaaaag ggaaatgagg 2889
267 aggagagtag aaaccacagc tcttagtagt aatggcatat agtctagagg accattcatg 2949
269 caatgactat ttctaaagca cctgctacac agcaggctgt acacagcaga tcagtactgt 3009
271 tcaacagaaac ttcttgagat gatggaaatg ttctacctct gcactcactg tccagtacat 3069
273 tagacactag gcacattggc tggttaatcac ttggaatgtg tttagcttga ctgaggaatt 3129
275 aaattttgat tgtaaattta aatcgccaca catggctagt ggctactgta ttggagtgc 3189
277 cagctctaga tggctcctag attattgaga gcctccaaaa caaatcaacc tagttctata 3249
279 gatgaagaca taaaagacac tggtaaacac caatgtaaaa gggcccccaa ggtggtcatg 3309
281 actggtctca ttgcagaag tctaagaatg tacctttttc tggccgggcg tggtagctca 3369
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293 <221> NAME/KEY: exon
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299 1 5 10 15
301 ctg tcc agg cag ggc gct gcc tgc aga acc agt gag tgc tgt ttt cag 96
302 Leu Ser Arg Gln Gly Ala Ala Cys Arg Thr Ser Glu Cys Cys Phe Gln
303 20 25 30
305 gac ccg cca tat ccg gat gca gac tca ggc tcg gcc tcg ggc cct agg 144
306 Asp Pro Pro Tyr Pro Asp Ala Asp Ser Gly Ser Ala Ser Gly Pro Arg
307 35 40 45
309 gac ctg aga tgc tat ccg ata tcc agt gat cgt tac gag tgc tcc tgg 192
310 Asp Leu Arg Cys Tyr Arg Ile Ser Ser Asp Arg Tyr Glu Cys Ser Trp
311 50 55 60
313 cag tat gag ggt ccc aca gct ggg gtc agc cac ttc ctg cgg tgt tgc 240
314 Gln Tyr Glu Gly Pro Thr Ala Gly Val Ser His Phe Leu Arg Cys Cys
315 65 70 75 80
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318 Leu Ser Ser Gly Arg Cys Cys Tyr Phe Ala Ala Gly Ser Ala Thr Arg
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322 Leu Gln Phe Ser Asp Gln Ala Gly Val Ser Val Leu Tyr Thr Val Thr
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327 115 120 125
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VERIFICATION SUMMARY

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L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date